

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT:
(A) NAME: Mitotix, Inc.
(B) STREET: One Kendall Square, Building 600
(C) CITY: Cambridge
(D) STATE: MA
10 (E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02139
(G) TELEPHONE: (617) 225-0001
(H) TELEFAX: (617) 225-0005
- 15 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
Human Pathogens, and Uses Related Thereto
- (iii) NUMBER OF SEQUENCES: 12
- 20 (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)
- 25 (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/463,090
(B) FILING DATE: 05-JUN-1995

30 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1668 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 40 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 259..1491

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATGATACA AATGTGGAAG ATGCAAATTG TTCTTCCCCT ACTTTGATGA GAAAAAGTGC 60

50 ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAATAATT CCAAATCACC ATCGCCAACT 120

TTTTCAAATA CAAATGCAAC ATCTGGCTCT CCATTGTCAA ATCTTTCTCG TGCACCATTG 180

AGAAATTTAT CTAATTTTCGT TATTCCTTCG TCAGTTAAAT CAAAAACGAA ACAATTTACA 240

55 AACTCTTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA 291

Met Thr Glu Val Val Ser Lys Ser Ser His Ser

1 5 10

	TTT TTC AAT AAT TTG CAT CTT GCA ACC TCA ACT GCG TCT TCT TCA GTA	339
	Phe Phe Asn Asn Leu His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val	
	15 20 25	
5	TCG AGC ACA ACT CCC AAA ATA GAA TTC AAT TCC ATA GCT GAA AAT GAT	387
	Ser Ser Thr Thr Pro Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp	
	30 35 40	
10	GAT ATC CCT ACC AAT TAT GAC TCT GAT GAA GAA TTC GAA GAT GGT GAT	435
	Asp Ile Pro Thr Asn Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp	
	45 50 55	
15	ACG TTT ATA CAA TCC ACC TTG ATT CAC CAG TTC AAC GCA AGT CAA GTA	483
	Thr Phe Ile Gln Ser Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val	
	60 65 70 75	
20	ACA ACA ACA ACA ATA ATA ATA ATA CCA ATG ATG GTA ACG ACA ATA ATA	531
	Thr Thr Thr Thr Ile Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile	
	80 85 90	
25	TAC CTA CAA AAA TTA GAC GGT TCC ACT CCA TGT ACC AAA CCG ATA AAG	579
	Tyr Leu Gln Lys Leu Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys	
	95 100 105	
30	AGA TTG CAT CGT ACC AAC TTC ATG AAG ATA ATT CAT TTT GAA ATT TAC	627
	Arg Leu His Arg Thr Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr	
	110 115 120	
35	AAT ATT GAA TAT TCT CAT CTG GAG AGT GAT TTG TTA CCA CGA ATC GAT	675
	Asn Ile Glu Tyr Ser His Ser Glu Ser Asp Leu Leu Pro Arg Ile Asp	
	125 130 135	
40	GCT CAT CAA TTA GCC AGA ATA TTA CGT GGA GAC CAC GAT GAC CAA TTT	723
	Ala His Gln Leu Ala Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe	
	140 145 150 155	
45	GAT GAA TTT ATT ATC ATT GAT TGT CGA TTT GAG TAT GAA TTT AAT GGT	771
	Asp Glu Phe Ile Ile Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly	
	160 165 170	
50	GGC CAT ATT ACT AGG GCA ATC AAT ATC TCC ACC CAG GAA GCA CTT CAA	819
	Gly His Ile Thr Arg Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln	
	175 180 185	
55	GAA AAG CTC TTT CAA TAT CAA GAA ACA GAT ACC AAG GAC ACT GAA AGC	867
	Glu Lys Leu Phe Gln Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser	
	190 195 200	
60	AAG AAG CGA TTG ATA ATT TTC CAT TGT GAG TTC AGT ATG TTC AGA GGA	915
	Lys Lys Arg Leu Ile Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly	
	205 210 215	
65	CCA ATG ATG GCC AAA CAT TTA AGA AAG TGT GAT AGA ATG TGC AAC TAC	963
	Pro Met Met Ala Lys His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr	
	220 225 230 235	
70	GAC AAT TAT CCT CTA TTA ACA TAC CCC GAT ATT GCA ATT TTG GAA GGA	1011
	Asp Asn Tyr Pro Leu Leu Thr Tyr Pro Asp Ile Ala Ile Leu Glu Gly	
	240 245 250	

0007294 05059

5 GGC TAT AAG AAT TTC TAT GAA AAT TAC CCC CAA TGG TGT GAT CCT CAA 1059
Gly Tyr Lys Asn Phe Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln
255 260 265

10 GGA TAT GTC GAG ATG AAG AAT TTA CGA CAC AAA AAA TTA TGT GAA TCC 1107
Gly Tyr Val Glu Met Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser
270 275 280

15 AAC TTG GAT AAA GTT AGA AAA GAT AAT AAA CTA ACT AGA GCA AAG TCT 1155
Asn Leu Asp Lys Val Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser
285 290 295

20 TAT CAA TTT GGT ATT CAA CAC CGC CGT GGT GGT TCC ACT GGT GGA CTT 1203
Tyr Gln Phe Gly Ile Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu
300 305 310 315

25 TTC GGC AAC TAT AAT TAC AAC GTT ATG AAC TCA TCA GAT CAA CAA TTT 1251
Phe Gly Asn Tyr Asn Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe
320 325 330

30 TGG AGT AGC AGT ACT TCC AAC ACT GCT CAC CAC AGA AGT AGT AGC AGT 1299
Trp Ser Ser Ser Thr Ser Asn Thr Ala His His Arg Ser Ser Ser Ser
335 340 345

35 AGC GGG TTC ATT AAT AAT ATG CAT AGT GGT GCT TCG TCA TAT CAC CAT 1347
Ser Gly Phe Ile Asn Asn Met His Ser Gly Ala Ser Ser Tyr His His
350 355 360

40 AGG TCA CAA TCG TTT GTA ACT ATC AAT AAT GAG AAA ATT ATC AAG CGA 1395
Arg Ser Gln Ser Phe Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg
365 370 375

45 CAA AGA TCG ACT CCC AAA GTC AGC AAC TCA CCA ACC AAG CCA CCT CAT 1443
Gln Arg Ser Thr Pro Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His
380 385 390 395

50 CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT 1491
Gln Ser Tyr Leu Ser Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp
400 405 410

55 TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT 1551

60 CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT 1611

65 CTGAATTATC AGTCAATACT CAAGATTTTC AACCAACCGAC TACGTCCTTT AGGAATT 1668

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS
(B) LOCATION: 208..513

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2:

	AACTTGTTTA CTTATTTGTT TATATAATTG ATAGATATCA ATTACTAATT TACCCTTGTT	60
10	TTTACTTCC TACTATTCAA GACTTTATTT CCTCTGATA ATCATTTTGT TTGATTATCA	120
	TTTTCGTCAA TTAGTTCCTTT TTTTTCATTT GTTCCAGAG TTTAGGAAGA CTACCATTTT	180
15	ACAATTTTCA ATTCAAATAT TTTCCCA ATG ACT AAA CCA AGA TTT TTA ACA Met Thr Lys Pro Arg Phe Leu Thr 1 5	231
20	AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC Arg Tyr Arg Lys Ser Lys Ser Val Gly Ile Ser Asp Met Ile His Tyr 10 15 20	279
25	AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu 25 30 35 40	327
30	CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu 45 50 55	375
35	ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA GAA TGG AGA GGG TTA GGA Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly 60 65 70	423
40	ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu 75 80 85	471
45	CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln 90 95 100	513
50	TAAAAAGATT AACTATATTT GAATACTATA GAATCGGAAT CGGTTTTAAA GTTAACACTG	573
55	GAATTAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA	633
60	CCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTTGTATA CACTATTTAT	693
65	AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA	753
70	AACTGTATAA ATACTCTTGG TACCTCGCAT GTT	786

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 43..993

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	TAGAACACAC	ACATCCCAAG	CCAAGACCAA	CACTTATTGC	AA	ATG	GTA	GAG	TTA		54						
						Met	Val	Glu	Leu								
						1											
15	TCT	GAT	TAT	CAA	CGT	CAA	GAA	AAA	GTC	GGA	GAA	GGT	ACT	TAT	GGG	GTT	102
	Ser	Asp	Tyr	Gln	Arg	Gln	Glu	Lys	Val	Gly	Glu	Gly	Thr	Tyr	Gly	Val	
	5					10				15						20	
20	GTT	TAT	AAA	GCA	TTA	GAT	ACC	AAG	CAC	AAT	AAT	AGA	GTT	GTT	GCA	TTA	150
	Val	Tyr	Lys	Ala	Leu	Asp	Thr	Lys	His	Asn	Asn	Arg	Val	Val	Ala	Leu	
					25					30					35		
25	AAG	AAA	ATT	CGA	TTA	GAA	TCA	GAA	GAT	GAA	GGT	GTA	CCT	AGT	ACC	GCC	198
	Lys	Lys	Ile	Arg	Leu	Glu	Ser	Glu	Asp	Glu	Gly	Val	Pro	Ser	Thr	Ala	
				40					45				50				
30	ATT	AGA	GAA	ATC	TCG	TTA	TTA	AAA	GAA	ATG	AAA	GAT	GAT	AAT	ATC	GTT	246
	Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Met	Lys	Asp	Asp	Asn	Ile	Val	
			55					60					65				
35	CGA	TTA	TAT	GAT	ATT	ATT	CAT	TCA	GAT	TCT	CAT	AAA	TTA	TAT	TTA	GTA	294
	Arg	Leu	Tyr	Asp	Ile	Ile	His	Ser	Asp	Ser	His	Lys	Leu	Tyr	Leu	Val	
		70					75					80					
40	TTT	GAA	TTT	TTG	GAT	TTA	GAT	TTA	AAG	AAA	TAT	ATG	GAA	AGT	ATT	CCT	342
	Phe	Glu	Phe	Leu	Asp	Leu	Asp	Leu	Lys	Lys	Tyr	Met	Glu	Ser	Ile	Pro	
	85				90					95					100		
45	CAA	GGA	GTT	GGA	CTA	GGG	GCT	AAT	ATG	ATA	AAA	AGA	TTT	ATG	AAT	CAA	390
	Gln	Gly	Val	Gly	Leu	Gly	Ala	Asn	Met	Ile	Lys	Arg	Phe	Met	Asn	Gln	
					105					110					115		
50	TTA	ATT	CGA	GGT	ATT	AAA	CAT	TGT	CAT	TCT	CAT	CGA	GTT	TTA	CAT	CGT	438
	Leu	Ile	Arg	Gly	Ile	Lys	His	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	
			120					125					130				
55	GAT	TTA	AAA	CCA	CAA	AAT	TTA	TTG	ATT	GAT	AAA	GAA	GGG	AAT	TTA	AAA	486
	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asp	Lys	Glu	Gly	Asn	Leu	Lys	
			135				140					145					
60	TTA	GCA	GAT	TTT	GGA	TTA	GCT	CGA	GCA	TTT	GGA	GTT	CCA	TTA	AGA	GCA	534
	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Leu	Arg	Ala	
		150					155					160					
65	TAT	ACT	CAT	GAA	GTT	GTC	ACT	TTA	TGG	TAT	CGA	GCT	CCC	GAA	ATC	TTG	582
	Tyr	Thr	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	
	165					170				175						180	

005050-1662060

	TTA GGA GGG AAA CAA TAT TCC ACT GGG GTA GAT ATG TGG TCT GTT GGA	630
	Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met Trp Ser Val Gly	
	185 190 195	
5	TGT ATA TTT GCT GAA ATG TGT AAT AGG AAA CCA TTA TTT CCT GGT GAT	678
	Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu Phe Pro Gly Asp	
	200 205 210	
10	TCA GAA ATT GAT GAA ATT TTC CGA ATT TTC CGA ATT TTA GGA ACA CCT	726
	Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile Leu Gly Thr Pro	
	215 220 225	
15	AAT GAA GAA ATT TGG CCT GAT GTT AAT TAT TTA CCA GAT TTT AAA TCA	774
	Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro Asp Phe Lys Ser	
	230 235 240	
20	AGT TTC CCT CAA TGG AAA AAG AAA CCT TTG AGT GAA GCA GTT CCA AGT	822
	Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu Ala Val Pro Ser	
	245 250 255 260	
25	TTG GAT GCT AAT GGA ATT GAT CTT TTG GAT CAA ATG TTG GTG TAT GAT	870
	Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met Leu Val Tyr Asp	
	265 270 275	
30	CCA AGT AGA AGA ATA AGT GCT AAA CGA GCT TTA ATT CAT CCT TAT TTT	918
	Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile His Pro Tyr Phe	
	280 285 290	
35	AAT GAT AAT GAT GAT CGT GAT CAT AAC AAT TAT AAT GAA GAT AAT ATT	966
	Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn Glu Asp Asn Ile	
	295 300 305	
40	GGG ATT GAC AAA CAC CAA AAC ATG CAA TAAATCTTG	1002
	Gly Ile Asp Lys His Gln Asn Met Gln	
	310 315	

(2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1752 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 184..1659

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTATTCCCC CTTTTTCCTT TTTTTTATAG AGAAACTTAT TCCAATTACT CATCGAACAA	60
GATCTTACTA GACTTGTAGA CTCACGACAC GATAAATTTT AATTCATTAA TCAACCAACG	120

	AACCAGCCAA ACCAAAATTA ATTCACATTT ATACTCACTG TTTGTTCATT TCATCTCATA																180
5	GTA	ATG	CCA	CAA	GTC	ACT	AAA	ACT	AAT	AAT	GAA	AAT	GAG	TTT	AGA	CTT	228
	Met	Pro	Gln	Val	Thr	Lys	Thr	Asn	Asn	Glu	Asn	Glu	Phe	Arg	Leu		
	1					5				10					15		
10	ACT	AGA	TCA	AAA	GTA	CAG	CAT	CAA	GAG	TCG	ATA	AGT	ACC	ATC	AAA	AAT	276
	Thr	Arg	Ser	Lys	Val	Gln	His	Gln	Glu	Ser	Ile	Ser	Thr	Ile	Lys	Asn	
					20					25					30		
15	ACG	ACC	ATA	TCC	AAT	TCT	CAG	CAT	AAA	CAA	CAA	ACA	CAA	CAA	CAA	ATT	324
	Thr	Thr	Ile	Ser	Asn	Ser	Gln	His	Lys	Gln	Gln	Thr	Gln	Gln	Gln	Ile	
				35					40					45			
20	TCA	TCA	CCA	CCT	CAA	GTC	TCT	GTA	ACA	TCA	TCT	GAA	GGA	GTT	TCA	CAT	372
	Ser	Ser	Pro	Pro	Gln	Val	Ser	Val	Thr	Ser	Ser	Glu	Gly	Val	Ser	His	
			50					55					60				
25	GTC	AAT	ACA	CGT	CAA	TAT	TTG	GGT	GAT	GTT	TCA	AAT	CAA	TAC	ATA	ACA	420
	Val	Asn	Thr	Arg	Gln	Tyr	Leu	Gly	Asp	Val	Ser	Asn	Gln	Tyr	Ile	Thr	
		65					70					75					
30	AAT	GCT	AAA	CCA	ACA	AAT	AAA	AGA	AAA	CCA	TTG	GGT	GGA	GAC	AAT	GCC	468
	Asn	Ala	Lys	Pro	Thr	Asn	Lys	Arg	Lys	Pro	Leu	Gly	Gly	Asp	Asn	Ala	
		80				85					90					95	
35	CCT	CTA	CAA	AAA	CAA	CAG	CAT	AGA	CCA	TCT	AGA	CCA	ATA	CCC	ATT	GCC	516
	Pro	Leu	Gln	Lys	Gln	Gln	His	Arg	Pro	Ser	Arg	Pro	Ile	Pro	Ile	Ala	
					100					105					110		
40	AGT	GAT	AAC	AAC	AAT	AAT	GGT	AGT	ACC	AGT	AGC	AGT	AGC	AAC	AGT	AGC	564
	Ser	Asp	Asn	Asn	Asn	Asn	Gly	Ser	Thr	Ser	Ser	Ser	Ser	Asn	Ser	Ser	
				115					120					125			
45	AAC	AAC	AAT	AAC	AAC	GAC	GCA	AAT	AGA	CTA	GCA	TCT	TTG	GCA	GTT	CCA	612
	Asn	Asn	Asn	Asn	Asn	Asp	Ala	Asn	Arg	Leu	Ala	Ser	Leu	Ala	Val	Pro	
			130					135					140				
50	TCT	CGA	TTA	CCC	CAA	AAA	CGA	CAA	GCT	ACT	GAA	TCG	TCG	ACA	AAT	TTA	660
	Ser	Arg	Leu	Pro	Gln	Lys	Arg	Gln	Ala	Thr	Glu	Ser	Ser	Thr	Asn	Leu	
		145					150					155					
55	GTA	GAG	AAA	TTA	AGA	GTA	CCA	CAA	CCA	GAA	GTA	GGG	GAA	AGA	AGT	CAG	708
	Val	Glu	Lys	Leu	Arg	Val	Pro	Gln	Pro	Glu	Val	Gly	Glu	Arg	Ser	Gln	
	160					165				170						175	
60	TCA	TAC	CAT	AAG	AAA	TCA	CGT	TTA	ATT	GAT	TAT	GAA	TGG	CAG	GAT	TTG	756
	Ser	Tyr	His	Lys	Lys	Ser	Arg	Leu	Ile	Asp	Tyr	Glu	Trp	Gln	Asp	Leu	
					180					185					190		
65	GAT	GAA	GAA	GAT	AAT	GAC	GAC	CAA	TTA	ATG	GTT	AGT	GAA	TAT	GTT	AAC	804
	Asp	Glu	Glu	Asp	Asn	Asp	Asp	Gln	Leu	Met	Val	Ser	Glu	Tyr	Val	Asn	
				195					200					205			
70	GAA	ATA	TTT	TCG	TAC	TAT	TAC	GAA	TTA	GAA	ACA	CGA</					

	Pro	Gln	Tyr	Leu	Phe	Lys	Gln	Thr	Leu	Leu	Lys	Pro	Arg	Met	Arg	Ser	
	225						230					235					
5	ATA	TTG	GTT	GAT	TGG	CTT	GTT	GAA	ATG	CAT	TTA	AAA	TTC	AAG	TTA	TTA	948
	Ile	Leu	Val	Asp	Trp	Leu	Val	Glu	Met	His	Leu	Lys	Phe	Lys	Leu	Leu	
	240					245					250					255	
10	CCT	GAA	TCA	CTT	TTT	TTG	GCA	GTC	AAT	GTA	ATG	GAT	AGA	TTC	ATG	TCT	996
	Pro	Glu	Ser	Leu	Phe	Leu	Ala	Val	Asn	Val	Met	Asp	Arg	Phe	Met	Ser	
				260						265					270		
15	GTT	GAA	GTG	GTT	CAA	ATA	GAT	AAA	TTA	CAA	TTA	TTG	GCT	ACA	GCA	GCT	1044
	Val	Glu	Val	Val	Gln	Ile	Asp	Lys	Leu	Gln	Leu	Leu	Ala	Thr	Ala	Ala	
				275					280					285			
20	TTA	TTT	ACT	GCT	GCC	AAA	AAT	GAA	GAA	GTA	TTT	TCT	CCC	CTG	GTT	AAA	1092
	Leu	Phe	Thr	Ala	Ala	Lys	Asn	Glu	Glu	Val	Phe	Ser	Pro	Ser	Val	Lys	
			290					295					300				
25	AAT	TAT	GCA	TAT	TTC	ACT	GAT	GGT	TCA	TAT	ACT	CCA	GAA	GAA	GTG	GTA	1140
	Asn	Tyr	Ala	Tyr	Phe	Thr	Asp	Gly	Ser	Tyr	Thr	Pro	Glu	Glu	Val	Val	
		305					310					315					
30	CAA	GCA	GAA	AAA	TAC	ATG	CTT	ACC	ATT	CTT	AAC	TTT	GAT	TTG	AAT	TAC	1188
	Gln	Ala	Glu	Lys	Tyr	Met	Leu	Thr	Ile	Leu	Asn	Phe	Asp	Leu	Asn	Tyr	
	320					325					330					335	
35	CCC	AAT	CCA	ATG	AAT	TTC	TTG	AGA	AGA	ATT	TCT	AAA	GCT	GAT	GAT	TAT	1236
	Pro	Asn	Pro	Met	Asn	Phe	Leu	Arg	Arg	Ile	Ser	Lys	Ala	Asp	Asp	Tyr	
					340					345					350		
40	GAT	GTC	CAA	TCA	AGA	ACG	CTA	GGA	AAA	TAT	CTT	TTG	GAA	ATC	ACT	ATA	1284
	Asp	Val	Gln	Ser	Arg	Thr	Leu	Gly	Lys	Tyr	Leu	Leu	Glu	Ile	Thr	Ile	
				355				360						365			
45	GTT	GAT	TAC	AAA	TTT	ATT	GGT	ATG	AGA	CCA	TCT	TTA	TGT	TGT	GCC	CTG	1332
	Val	Asp	Tyr	Lys	Phe	Ile	Gly	Met	Arg	Pro	Ser	Leu	Cys	Cys	Ala	Ser	
			370				375						380				
50	GCC	ATG	TAT	TTA	GCA	AGA	CTA	ATA	TTG	GGC	AAA	TTG	CCA	GTT	TGG	AAT	1380
	Ala	Met	Tyr	Leu	Ala	Arg	Leu	Ile	Leu	Gly	Lys	Leu	Pro	Val	Trp	Asn	
		385					390					395					
55	GGG	AAT	TTG	ATT	CAT	TAT	AGT	GGA	GGT	TAT	AGA	ATC	AGT	GAT	ATG	AGA	1428
	Gly	Asn	Leu	Ile	His	Tyr	Ser	Gly	Gly	Tyr	Arg	Ile	Ser	Asp	Met	Arg	
	400					405					410					415	
60	GAA	TGT	ATC	GAA	TTA	ATG	TTT	CAA	TAT	CTT	ATT	GCT	CCT	ATA	GAA	CAT	1476
	Glu	Cys	Ile	Glu	Leu	Met	Phe	Gln	Tyr	Leu	Ile	Ala	Pro	Ile	Glu	His	
					420					425					430		
65	GAT	GAA	TTT	TTC	AAA	AAA	TAT	GCC	ATG	AGA	AAA	TTT	ATG	AGA	GCA	AGT	1524
	Asp	Glu	Phe	Phe	Lys	Lys	Tyr	Ala	Met	Arg	Lys	Phe	Met	Arg	Ala	Ser	
				435				440					445				
70	ACT	CTT	TGT	CGA	AAT	TGG	GCT	AAA	AAA	TTC	CAA	GCA	TCA	GGA	AGA	GAT	1572
	Thr	Leu	Cys	Arg	Asn	Trp	Ala	Lys	Lys	Phe	Gln	Ala	Ser	Gly	Arg	Asp	
			450				455						460				

00072094-050619

TTG TTT GAT GAA CGA TTA TCG ACC CAT AGG CTA ACA TTA GAA GAT GAT 1620
 Leu Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp
 465 470 475

5 GAC GAA GAA GAA GAA ATA GTG GTA GCA GAA GCA GAA GAG TAAAGTTTGT 1669
 Asp Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu
 480 485 490

10 AGGACTATTG GATCTAGGTT CTTATCTTTA CAATGCATAA ATGAGGAAAT GAAAGAAGAT 1729
 GAACATGAGT TATGTGCATT ACC 1752

15 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1070 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 30..1058

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCAAAATCCA TCAGAGAACC ACATCAATC ATG TCT ACT GCA GCA GTT GCA ACG 53
 Met Ser Thr Ala Ala Val Ala Thr
 35 1 5

AAA CCA TCT GTC ACT TCA AAA CCA GCA ACT AAA CAA GTT CTG AAT TAC 101
 Lys Pro Ser Val Thr Ser Lys Pro Ala Thr Lys Gln Val Leu Asn Tyr
 10 15 20

40 ACC AAA GAA AAA AAA GTA GGG GAA GGT ACA TAT GCT GTT GTG TAC TTG 149
 Thr Lys Glu Lys Lys Val Gly Glu Gly Thr Tyr Ala Val Val Tyr Leu
 25 30 35 40

45 GGT AAA CAA ATC TCC ACC AAA CGT CAA ATT GCC ATC AAA GAA ATC AAA 197
 Gly Lys Gln Ile Ser Thr Lys Arg Gln Ile Ala Ile Lys Glu Ile Lys
 45 50 55

50 ACA GGA TTA TTC AAA GAT GGG TTG GAT ATG TCA GCA TTG AGA GAA GTG 245
 Thr Gly Leu Phe Lys Asp Gly Leu Asp Met Ser Ala Leu Arg Glu Val
 60 65 70

AAA TAT TTG CAA GAA TTG AAA CAT CCC AAT GTT ATT GAA CTA GTA GAT 293
 Lys Tyr Leu Gln Glu Leu Lys His Pro Asn Val Ile Glu Leu Val Asp
 55 75 80 85

GTA TTT TCA GCA ACA AAT AAT TTA AAT TTG GTA TTA GAA TTT CTA CCT 341
 Val Phe Ser Ala Thr Asn Asn Leu Asn Leu Val Leu Glu Phe Leu Pro
 90 95 100

BB5050: 16622060

340

1070

(2) INFORMATION FOR SEQ ID NO:6:

10

15

(A) NAME/KEY: CDS
(B) LOCATION: 1..477

20

25

30

35

40

45

50

55

GGG ACT TTA AAA ATA TGT GAT TTC GGC TTA GCA CGA GGA ATA AAT CCT 432
Gly Thr Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Ile Asn Pro
130 135 140

GTA TAT TTC AGA AAC CGC TCA GCT GTC ATC ACA AAC TAC GTA GCA
Val Tyr Phe Arg Asn Arg Ser Ala Val Ile Thr Asn Tyr Val Ala
145 150 155

5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Thr Glu Val Val Ser Lys Ser Ser His Ser Phe Phe Asn Asn Leu
1 5 10 15
His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val Ser Ser Thr Thr Pro
20 20 25 30
Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp Asp Ile Pro Thr Asn
35 40 45
Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp Thr Phe Ile Gln Ser
50 55 60
Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val Thr Thr Thr Thr Ile
65 70 75 80
Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile Tyr Leu Gln Lys Leu
85 90 95
Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys Arg Leu His Arg Thr
100 105 110
Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr Asn Ile Glu Tyr Ser
115 120 125
His Leu Glu Ser Asp Leu Leu Pro Arg Ile Asp Ala His Gln Leu Ala
130 135 140
Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe Asp Glu Phe Ile Ile
145 150 155 160
Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly Gly His Ile Thr Arg
165 170 175
Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln Glu Lys Leu Phe Gln
180 185 190
Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser Lys Lys Arg Leu Ile
195 200 205
Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly Pro Met Met Ala Lys
210 215 220
His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr Asp Asn Tyr Pro Leu

00072094-05060

5

10

15

20

25

30

35

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50

55

Met	Thr	Lys	Pro	Arg	Phe	Leu	Thr	Arg	Tyr	Arg	Lys	Ser	Lys	Ser	Val
1				5					10					15	
Gly	Ile	Ser	Asp	Met	Ile	His	Tyr	Ser	Pro	Arg	Tyr	Ser	Asp	Asp	Ser
			20					25					30		
Tyr	Glu	Tyr	Arg	His	Val	Met	Leu	Pro	Lys	Asn	Met	Leu	Lys	Ala	Ile
		35					40					45			
Pro	His	Asp	Tyr	Phe	Asn	Gln	Glu	Thr	Gly	Thr	Leu	Arg	Ile	Leu	Thr
	50					55					60				

Glu Glu Glu Trp Arg Gly Leu Gly Ile Thr Gln Ser Leu Gly Trp Ala
65 70 75 80
His Tyr Glu Thr His Ala Pro Glu Pro His Ile Leu Leu Phe Lys Arg
5 85 90 95
Pro Leu Asn Pro Gly Gln
100

10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Glu Leu Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly
1 5 10 15
25 Thr Tyr Gly Val Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg
20 25 30
Val Val Ala Leu Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val
35 40 45
30 Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp
50 55 60
35 Asp Asn Ile Val Arg Leu Tyr Asp Ile Ile His Ser Asp Ser His Lys
65 70 75 80
Leu Tyr Leu Val Phe Glu Phe Leu Asp Leu Asp Leu Lys Lys Tyr Met
85 90 95
40 Glu Ser Ile Pro Gln Gly Val Gly Leu Gly Ala Asn Met Ile Lys Arg
100 105 110
Phe Met Asn Gln Leu Ile Arg Gly Ile Lys His Cys His Ser His Arg
115 120 125
45 Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asp Lys Glu
130 135 140
50 Gly Asn Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val
145 150 155 160
Pro Leu Arg Ala Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala
165 170 175
55 Pro Glu Ile Leu Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met
180 185 190
Trp Ser Val Gly Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu
195 200 205

36950-10622000

Phe Pro Gly Asp Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile
210 215 220

5 Leu Gly Thr Pro Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro
225 230 235 240

Asp Phe Lys Ser Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu
245 250 255

10 Ala Val Pro Ser Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met
260 265 270

Leu Val Tyr Asp Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile
275 280 285

15 His Pro Tyr Phe Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn
290 295 300

20 Glu Asp Asn Ile Gly Ile Asp Lys His Gln Asn Met Gln
305 310 315

(2) INFORMATION FOR SEQ ID NO:10:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35 Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu Thr
1 5 10 15

Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn Thr
20 25 30

40 Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Gln Ile Ser
35 40 45

Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His Val
50 55 60

Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr Asn
65 70 75 80

50 Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala Pro
85 90 95

Leu Gln Lys Gln Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala Ser
100 105 110

55 Asp Asn Asn Asn Asn Gly Ser Thr Ser Ser Ser Ser Asn Ser Ser Asn
115 120 125

Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro Ser

3699050-46622000

	130					135					140					
5	Arg 145	Leu	Pro	Gln	Lys	Arg 150	Gln	Ala	Thr	Glu	Ser 155	Ser	Thr	Asn	Leu 160	Val
	Glu	Lys	Leu	Arg	Val 165	Pro	Gln	Pro	Glu	Val 170	Gly	Glu	Arg	Ser	Gln 175	Ser
10	Tyr	His	Lys	Lys	Ser 180	Arg	Leu	Ile	Asp 185	Tyr	Glu	Trp	Gln	Asp 190	Leu	Asp
	Glu	Glu	Asp 195	Asn	Asp	Asp	Gln	Leu 200	Met	Val	Ser	Glu	Tyr 205	Val	Asn	Glu
15	Ile	Phe 210	Ser	Tyr	Tyr	Tyr	Glu 215	Leu	Glu	Thr	Arg 220	Met	Leu	Pro	Asp	Pro
	Gln 225	Tyr	Leu	Phe	Lys	Gln 230	Thr	Leu	Leu	Lys	Pro 235	Arg	Met	Arg	Ser	Ile 240
20	Leu	Val	Asp	Trp	Leu 245	Val	Glu	Met	His	Leu 250	Lys	Phe	Lys	Leu 255	Leu	Pro
	Glu	Ser	Leu	Phe 260	Leu	Ala	Val	Asn 265	Val	Met	Asp	Arg	Phe	Met 270	Ser	Val
25	Glu	Val	Val 275	Gln	Ile	Asp	Lys	Leu 280	Gln	Leu	Leu	Ala	Thr 285	Ala	Ala	Leu
30	Phe 290	Thr	Ala	Ala	Lys	Asn	Glu 295	Glu	Val	Phe	Ser 300	Pro	Leu	Val	Lys	Asn
	Tyr 305	Ala	Tyr	Phe	Thr	Asp 310	Gly	Ser	Tyr	Thr	Pro 315	Glu	Glu	Val	Val	Gln 320
35	Ala	Glu	Lys	Tyr	Met 325	Leu	Thr	Ile	Leu	Asn 330	Phe	Asp	Leu	Asn	Tyr 335	Pro
	Asn	Pro	Met	Asn 340	Phe	Leu	Arg	Arg	Ile 345	Ser	Lys	Ala	Asp	Asp 350	Tyr	Asp
40	Val	Gln	Ser 355	Arg	Thr	Leu	Gly	Lys 360	Tyr	Leu	Leu	Glu	Ile 365	Thr	Ile	Val
45	Asp 370	Tyr	Lys	Phe	Ile	Gly	Met 375	Arg	Pro	Ser	Leu	Cys 380	Cys	Ala	Leu	Ala
	Met 385	Tyr	Leu	Ala	Arg	Leu 390	Ile	Leu	Gly	Lys	Leu 395	Pro	Val	Trp	Asn	Gly 400
50	Asn	Leu	Ile	His	Tyr 405	Ser	Gly	Gly	Tyr	Arg 410	Ile	Ser	Asp	Met	Arg 415	Glu
	Cys	Ile	Glu	Leu 420	Met	Phe	Gln	Tyr	Leu 425	Ile	Ala	Pro	Ile 430	Glu	His	Asp
55	Glu	Phe	Phe 435	Lys	Lys	Tyr	Ala	Met 440	Arg	Lys	Phe	Met	Arg 445	Ala	Ser	Thr

[illegible]

(2) INFORMATION FOR SEQ ID NO:11:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	Met	Ser	Thr	Ala	Ala	Val	Ala	Thr	Lys	Pro	Ser	Val	Thr	Ser	Lys	Pro
	1				5					10					15	
25	Ala	Thr	Lys	Gln	Val	Leu	Asn	Tyr	Thr	Lys	Glu	Lys	Lys	Val	Gly	Glu
				20					25					30		
	Gly	Thr	Tyr	Ala	Val	Val	Tyr	Leu	Gly	Lys	Gln	Ile	Ser	Thr	Lys	Arg
30			35					40					45			
	Gln	Ile	Ala	Ile	Lys	Glu	Ile	Lys	Thr	Gly	Leu	Phe	Lys	Asp	Gly	Leu
		50					55					60				
35	Asp	Met	Ser	Ala	Leu	Arg	Glu	Val	Lys	Tyr	Leu	Gln	Glu	Leu	Lys	His
	65					70					75					80
	Pro	Asn	Val	Ile	Glu	Leu	Val	Asp	Val	Phe	Ser	Ala	Thr	Asn	Asn	Leu
					85					90					95	
40	Asn	Leu	Val	Leu	Glu	Phe	Leu	Pro	Cys	Asp	Leu	Glu	Val	Leu	Ile	Lys
				100					105					110		
	Asp	Lys	Ser	Ile	Val	Phe	Lys	Ser	Ala	Asp	Ile	Lys	Ser	Trp	Leu	Leu
45			115					120					125			
	Met	Thr	Leu	Arg	Gly	Ile	His	His	Cys	His	Arg	Asn	Phe	Ile	Leu	His
		130					135					140				
50	Arg	Asp	Leu	Lys	Pro	Asn	Asn	Leu	Leu	Leu	Ala	Pro	Asp	Gly	Gln	Leu
	145					150					155					160
	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Leu	Val	Asn	Pro	Asn	Glu
					165					170					175	
55	Asp	Leu	Ser	Ser	Asn	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Leu
				180					185					190		
	Leu	Phe	Gly	Ala	Arg	His	Tyr	Thr	Gly	Ala	Val	Asp	Ile	Trp	Ser	Ile

195 200 205

5 Gly Ile Ile Phe Ala Glu Leu Met Leu Arg Ile Pro Tyr Leu Pro Gly
210 215 220

Lys Asp Asp Val Asp Gln Leu Asp Val Thr Phe Arg Ala Tyr Gly Thr
225 230 235 240

10 Pro Thr Glu Gln Ile Trp Pro Asn Val Ser Ser Leu Pro Met Tyr Asn
245 250 255

Ala Leu His Val Tyr Pro Pro Pro Ser Arg Gln Glu Leu Arg Asn Arg
260 265 270

15 Phe Ser Ala Ala Thr Glu Lys Ala Leu Asp Leu Leu Ile Ser Met Thr
275 280 285

Gln Leu Asp Pro Ser Arg Arg Cys Asp Ser Thr Leu Ala Leu Leu His
290 295 300

20 Asp Tyr Phe Thr Glu Ser Pro Arg Pro Thr Asp Pro Lys Lys Leu Pro
305 310 315 320

25 Lys Lys Ser Ser Pro Glu Lys Arg Glu Asn Glu Asp Glu Gln Asn Asn
325 330 335

Gly Ser Lys Arg Arg His Val
340

30 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

40 Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys
1 5 10 15

45 Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu
20 25 30

Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His
35 40 45

50 Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro
50 55 60

Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala
65 70 75 80

55 Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser
85 90 95

009050-16022000

5	Val	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Ile	Leu	Val	Thr	Thr	Gln
			115					120					125			
	Gly	Thr	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Gly	Ile	Asn	Pro
			130				135					140				
10	Val	Tyr	Phe	Arg	Asn	Arg	Ser	Ala	Val	Ile	Thr	Asn	Tyr	Val	Ala	
	145					150					155					

15

20

25

30

35

40

50

55

60

65

ATC AAA TTA TGG TTA AAA TCA ATG AGT TCA GGA CTT GAA TTT ATT CAT 432
Ile Lys Leu Trp Leu Lys Ser Met Ser Ser Gly Leu Glu Phe Ile His

	130				135				140								
5	TCA	CAA	GGG	ATA	ATT	CAT	CGT	GAT	ATA	AAA	CCC	AGT	AAT	ATT	TTC	TTT	480
	Ser	Gln	Gly	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Phe	Phe	
	145					150					155					160	
10	GCC	CGG	GAT	GAT	ATA	ACA	CAA	CCG	ATT	ATT	GGA	GAT	TTT	GAT	ATT	TGT	528
	Ala	Arg	Asp	Asp	Ile	Thr	Gln	Pro	Ile	Ile	Gly	Asp	Phe	Asp	Ile	Cys	
					165					170					175		
15	TAT	GAT	TTA	AAA	CTG	CCA	CCT	AAA	GAT	GAA	CCC	CCT	ATG	GCG	AAA	TAT	576
	Tyr	Asp	Leu	Lys	Leu	Pro	Pro	Lys	Asp	Glu	Pro	Pro	Met	Ala	Lys	Tyr	
				180					185					190			
20	ATT	GAT	GTA	TCT	ACA	GGT	ATT	TAT	AAA	GCA	CCA	GAA	TTG	ATT	CTT	GGT	624
	Ile	Asp	Val	Ser	Thr	Gly	Ile	Tyr	Lys	Ala	Pro	Glu	Leu	Ile	Leu	Gly	
			195					200					205				
25	ATA	ACT	AAT	TAT	GAA	TAT	GAA	ATT	GAT	ATT	TGG	TCA	TTG	GGT	ATA	ATT	672
	Ile	Thr	Asn	Tyr	Glu	Tyr	Glu	Ile	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Ile	
			210				215					220					
30	TTG	ACT	GGT	TTA	TAT	TCA	GAA	AAT	TTT	CAA	AGT	GTT	TTA	GTC	AAA	GAT	720
	Leu	Thr	Gly	Leu	Tyr	Ser	Glu	Asn	Phe	Gln	Ser	Val	Leu	Val	Lys	Asp	
	225					230					235					240	
35	GAT	AAA	GAA	TTG	ACT	AAT	GAT	TCT	CAT	GTT	AGT	GAT	TTA	TAT	TTA	TTA	768
	Asp	Lys	Glu	Leu	Thr	Asn	Asp	Ser	His	Val	Ser	Asp	Leu	Tyr	Leu	Leu	
				245						250					255		
40	AAT	CAA	ATA	TTT	GAA	AAT	TTC	GGT	ACA	CCC	AAT	TTA	ACT	GAT	TTT	GAA	816
	Asn	Gln	Ile	Phe	Glu	Asn	Phe	Gly	Thr	Pro	Asn	Leu	Thr	Asp	Phe	Glu	
				260					265					270			
45	GAT	GAA	TTA	TTT	TGT	GAT	GAA	TAT	AAT	AAT	GAA	AAC	TTG	CAT	TTT	AAA	864
	Asp	Glu	Leu	Phe	Cys	Asp	Glu	Tyr	Asn	Asn	Glu	Asn	Leu	His	Phe	Lys	
			275					280					285				
50	AAA	TTC	AAT	TTA	CAA	AAA	TAT	CCT	AGA	AAA	GAT	TGG	GAT	ATT	ATT	TTA	912
	Lys	Phe	Asn	Leu	Gln	Lys	Tyr	Pro	Arg	Lys	Asp	Trp	Asp	Ile	Ile	Leu	
			290				295					300					
55	CCT	CGA	TGC	AAT	GAT	GAT	TTA	ATG	AAA	GAA	ATT	TTT	ACC	AAG	ATG	ATT	960
	Pro	Arg	Cys	Asn	Asp	Asp	Leu	Met	Lys	Glu	Ile	Phe	Thr	Lys	Met	Ile	
	305					310					315					320	
60	AGA	TAT	GAT	CGA	AGT	AAA	AGA	ATA	ACT	TCT	AAA	GAA	ATC	TTA	CAA	TTA	1008
	Arg	Tyr	Asp	Arg	Ser	Lys	Arg	Ile	Thr	Ser	Lys	Glu	Ile	Leu	Gln	Leu	
					325					330					335		
65	ATG	TTG	GAT	TG													1019
	Met	Leu	Asp														

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Leu Ser Asp Tyr Tyr Ile Asp Lys Glu Leu Ile Tyr Asn Ser

[illegible]